purified pcr product (200ng) was ligated into the srf I site of the plasmid PCR-Script cloning vector and the resultant plasmid was used to transform E.coli DH10 cells. Colonies containing the 1.2kb NotI fragment were identified by antibiotic (ampicillin selection) and blue / white (IPTG + X-gal) selection of colonies on LB/Amp plates. White (recombinant) colonies were picked and grown overnight on liquid LB/Amp culture. Positive clones were identified by plasmid preparation and restriction digest analysis for the presence of the 1.2kB NotI fragment. Positive clones were used as template to fully sequence the phytyl transferase of (both strands). Plasmids containing the correct insert verified by nucleic acid sequence were digested with NotI and the 1.2kb fragment ligated to NotI-digested and phosphatase-treated pKS67. The plasmid pKS67 was prepared by replacing in pRB20 (described in U.S. Patent No. 5,846,784) the 800 bp Nos 3' fragment, with the 285 bp Nos 3' fragment containing the polyadenylation signal sequence and described in Depicker et al. (1982) *J. Mol. Appl. Genet.* 1:561-573. Clones were screened for the sense and antisense orientation of the phytyl/prenyltransferase insert fragment by restriction enzyme digestion. --

B9

In the Claims:

Please cancel claims 1-21, 29, 30, 37, 38, and 39 without prejudice.

Please amend claims 22, 23, 24, 27, 28, 31, 32, 33, 34, 35, and 36 as follows:

22. (Amended) A method for modulating the level of phytyl/prenyltransferase protein in a plant, comprising:

B10

(a) stably transforming a plant cell with a phytyl/prenyltransferase polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation;

(b) growing the plant cell under plant growing conditions to produce a regenerated plant which expresses the polynucleotide for a time sufficient to modulate the level of phytyl/prenyltransferase protein in the plant.

23. (Amended) The method of claim 22, wherein the phytyl/prenyltransferase polynucleotide is SEQ ID NO: 3.

B10

24. (Amended) The method of claim 22, wherein the plant is corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, *Arabidopsis thaliana*, tomato, *Brassica,* pepper, potato, apple, spinach, or lettuce.

---

27. (Amended) A method for modulating the level of tocopherol in a plant, comprising:

(a) stably transforming a plant cell with a phytyl/prenyltransferase polynucleotide operably linked to a promoter, wherein the polynucleotide is in sense or antisense orientation;

B11

(b) growing the plant cell under plant growing conditions to produce a regenerated plant which expresses the polynucleotide for a time sufficient to modulate level of tocopherol in the plant.

28. (Amended) The method of claim 27, wherein the phytyl/prenyltransferase polynucleotide is SEQ ID NO: 3.

B12

31. (Amended) The method of claim 22, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:

(a) a polynucleotide having at least 70% sequence identity to the entire coding sequence of SEQ ID NO: 3, wherein the % sequence identity is determined by GAP using default parameters, and

(b) a polynucleotide complimentary to a polynucleotide of (a).

B12

32. (Amended) The method of claim 22, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:

(a) a polynucleotide that encodes a polypeptide of SEQ ID NO: 4;

(b) a polynucleotide comprising the sequence set forth in SEQ ID NO: 3; and

(c) a polynucleotide complementary to a polynucleotide of (a) or (b).

33. (Amended) The method of claim 22, wherein the phytyl/prenyltransferase polynucleotide comprises a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 2X SSC at 50°C, to a hybridization probe the polynucleotide sequence of which consists of the coding sequence of SEQ ID NO: 3.

34. (Amended) The method of claim 27, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:

(a) a polynucleotide having at least 70% sequence identity to the entire coding sequence of SEQ ID NO: 3, wherein the % sequence identity is determined by GAP using default parameters, and

(b) a polynucleotide complimentary to a polynucleotide of (a).

35. (Amended) The method of claim 27, wherein the phytyl/prenyltransferase polynucleotide comprises a member selected from the group consisting of:

(a) a polynucleotide that encodes a polypeptide of SEQ ID NO: 4;

(b) a polynucleotide comprising the sequence set forth in SEQ ID NO: 3; and

(c) a polynucleotide complementary to a polynucleotide of (a) or (b).

B12

36. (Amended) The method of claim 27, wherein the phytyl/prenyltransferase polynucleotide comprises a polynucleotide which selectively hybridizes, under stringent hybridization conditions and a wash in 2X SSC at 50°C, to a hybridization probe the polynucleotide sequence of which consists of the coding sequence of SEQ ID NO: 3, or the complement of the coding sequence of SEQ ID NO: 3.